

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/552, 014 A
Source: IFW0
Date Processed by STIC: 05/08/2006

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IFWO

RAW SEQUENCE LISTING

DATE: 05/08/2006

PATENT APPLICATION: US/10/552,014A

TIME: 10:53:45

Input Set : A:\3172us0pSeqCORR.txt

Output Set: N:\CRF4\05082006\J552014A.raw

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3 <110> APPLICANT: ITO, Yasuaki
4     FUJII, Ryo
5     KOBAYASHI, Makoto
6     HINUMA, Shuji
7     HASHIMOTO, Tadatoshi
8     TANAKA, Yasuhiro
10 <120> TITLE OF INVENTION: Novel Screening Method
12 <130> FILE REFERENCE: 3172US0P
14 <140> CURRENT APPLICATION NUMBER: 10/552,014A
15 <141> CURRENT FILING DATE: 2005-10-12
17 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/005947
18 <151> PRIOR FILING DATE: 2004-04-23
20 <150> PRIOR APPLICATION NUMBER: JP 2003-122464
21 <151> PRIOR FILING DATE: 2003-04-25
23 <160> NUMBER OF SEQ ID NOS: 15
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 453
27 <212> TYPE: PRT
28 <213> ORGANISM: Human
30 <400> SEQUENCE: 1
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33 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
34           20                      25                      30
35 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Met Gly Leu Leu Gly Asn
36           35                      40                      45
37 Ser Ala Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
38           50                      55                      60
39 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
40           65                      70                      75                      80
41 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
42           85                      90                      95
43 Asn Pro Leu Thr Thr Ser Ser Tyr Thr Leu Ser Cys Lys Leu His Thr
44           100                     105                     110
45 Phe Leu Phe Glu Ala Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
46           115                     120                     125
47 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Arg Tyr Lys
48           130                     135                     140
49 Ala Val Ser Gly Pro Cys Gln Val Lys Leu Leu Ile Gly Phe Val Trp
50           145                     150                     155                     160
51 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Thr
52           165                     170                     175
53 Glu Tyr Pro Leu Val Asn Val Pro Ser His Arg Gly Leu Thr Cys Asn

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54          180          185          190
55 Arg Ser Ser Thr Arg His His Glu Gln Pro Glu Thr Ser Asn Met Ser
56          195          200          205
57 Ile Cys Thr Asn Leu Ser Ser Arg Trp Thr Val Phe Gln Ser Ser Ile
58          210          215          220
59 Phe Gly Ala Phe Val Val Tyr Leu Val Val Leu Ser Val Ala Phe
60 225          230          235          240
61 Met Cys Trp Asn Met Met Gln Val Leu Met Lys Ser Gln Lys Gly Ser
62          245          250          255
63 Leu Ala Gly Gly Thr Arg Pro Pro Gln Leu Arg Lys Ser Glu Ser Glu
64          260          265          270
65 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
66          275          280          285
67 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
68          290          295          300
69 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Ser Tyr Phe Arg
70 305          310          315          320
71 Ala Tyr Met Ile Leu Leu Pro Phe Ser Glu Thr Phe Phe Tyr Leu Ser
72          325          330          335
73 Ser Val Ile Asn Pro Leu Leu Tyr Thr Val Ser Ser Gln Gln Phe Arg
74          340          345          350
75 Arg Val Phe Val Gln Val Leu Cys Cys Arg Leu Ser Leu Gln His Ala
76          355          360          365
77 Asn His Glu Lys Arg Leu Arg Val His Ala His Ser Thr Thr Asp Ser
78          370          375          380
79 Ala Arg Phe Val Gln Arg Pro Leu Leu Phe Ala Ser Arg Arg Gln Ser
80 385          390          395          400
81 Ser Ala Arg Arg Thr Glu Lys Ile Phe Leu Ser Thr Phe Gln Ser Glu
82          405          410          415
83 Ala Glu Pro Gln Ser Lys Ser Gln Ser Leu Ser Leu Glu Ser Leu Glu
84          420          425          430
85 Pro Asn Ser Gly Ala Lys Pro Ala Asn Ser Ala Ala Glu Asn Gly Phe
86          435          440          445
87 Gln Glu His Glu Val
88          450
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91 <211> LENGTH: 1359
92 <212> TYPE: DNA
93 <213> ORGANISM: Human
95 <400> SEQUENCE: 2
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97 cccgagtttg aggtggccac ctggatcaaa atcaccctta ttctggtgta cctgatcatc 120
98 ttcgtgatgg gccttctggg gaacagcgcc accattcggg tcaccaggt gctgcagaag 180
99 aaaggatact tgcagaagga ggtgacagac cacatggtga gtttggttg ctcggacatc 240
100 ttggtgttcc tcatcggcat gccatggag ttctacagca tcatctggaa tcccctgacc 300
101 acgtccagct acaccctgtc ctgcaagctg cacactttcc tcttcgaggc ctgcagctac 360
102 gctacgtctg tgcacgtgct gacactcagc tttgagcgct acatcgccat ctgtcaccct 420
103 ttcaggtaca aggtgtgtgc gggaccttgc caggtgaagc tgctgattgg cttcgtctgg 480
104 gtcacctccg ccctggtggc actgcccttg ctgtttgcca tgggtactga gtacccctg 540

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105 gtgaacgtgc ccagccaccg ggggtctcact tgcaaccgct ccagcaccgg ccaccacgag 600
106 cagcccagaga cctccaatat gtccatctgt accaacctct ccagccgctg gaccgtgttc 660
107 cagtccagca tcttcggcgc cttegtgtgc tacctcgtgg tcttgccttc cgtagccttc 720
108 atgtgctgga acatgatgca ggtgctcatg aaaagccaga agggctcgct ggccgggggc 780
109 acgcggcctc cgcagctgag gaagtccgag agcgaagaga gcaggaccgc caggaggcag 840
110 accatcatct tcctgaggct gattgttgtg acattggccg tatgctggat gccaaccag 900
111 attcggagga tcatggctgc ggccaaacc aagcacgact ggacgaggtc ctacttcgg 960
112 gcgtacatga tcctcctccc ctctcggag acgtttttct acctcagctc ggtcatcaac 1020
113 ccgctcctgt acacgggtgc ctgcgagcag ttccggcggg tggtcgtgca ggtgctgtgc 1080
114 tgccgcctgt cgctgcagca cgccaaccac gagaagcgcc tgcgcgta ca tgcgactcc 1140
115 accaccgaca gcgcccgtt tgtgcagcgc ccgttgctct tcgcgtcccg gcgccagtcc 1200
116 tctgcaagga gaactgagaa gattttctta agcacttttc agagcgaggc cgagccccag 1260
117 tctaagtccc agtcattgag tctcgagtca ctagagccca actcaggcgc gaaaccagcc 1320
118 aattctgctg cagagaatgg ttttcaggag catgaagtt 1359

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120 <210> SEQ ID NO: 3

121 <211> LENGTH: 20

122 <212> TYPE: DNA

123 <213> ORGANISM: Artificial Sequence

125 <220> FEATURE:

126 <223> OTHER INFORMATION: primer

128 <400> SEQUENCE: 3

129 tgtgacattg gccgtatgct 20

131 <210> SEQ ID NO: 4

132 <211> LENGTH: 19

133 <212> TYPE: DNA

134 <213> ORGANISM: Artificial Sequence

136 <220> FEATURE:

137 <223> OTHER INFORMATION: primer

139 <400> SEQUENCE: 4

140 cagtcgtgct tgggtttgg 19

142 <210> SEQ ID NO: 5

143 <211> LENGTH: 24

144 <212> TYPE: DNA

145 <213> ORGANISM: Artificial Sequence

147 <220> FEATURE:

148 <223> OTHER INFORMATION: primer

150 <400> SEQUENCE: 5

151 tgcccaacca gattcggagg atca 24

153 <210> SEQ ID NO: 6

155 <211> LENGTH: 456

156 <212> TYPE: PRT

157 <213> ORGANISM: Mouse

159 <400> SEQUENCE: 6

160 Met Ala Ser Ser Ser Gly Ser Asn His Ile Cys Ser Arg Val Ile Asp

161 5 10 15

162 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr

163 20 25 30

164 Leu Ile Leu Val Tyr Leu Ile Ile Phe Val Val Gly Ile Leu Gly Asn

165 35 40 45

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166 Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
167      50      55      60
168 Gln Lys Glu Val Thr Asp His Met Val Ser Leu Ala Cys Ser Asp Ile
169 65      70      75      80
170 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
171      85      90      95
172 Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr
173      100      105      110
174 Phe Leu Phe Glu Thr Cys Ser Tyr Ala Thr Leu Leu His Val Leu Thr
175      115      120      125
176 Leu Ser Phe Glu Arg Tyr Ile Ala Ile Cys His Pro Phe Lys Tyr Lys
177      130      135      140
178 Ala Val Ser Gly Pro Arg Gln Val Lys Leu Leu Ile Gly Phe Val Trp
179 145      150      155      160
180 Val Thr Ser Ala Leu Val Ala Leu Pro Leu Leu Phe Ala Met Gly Ile
181      165      170      175
182 Glu Tyr Pro Leu Val Asn Val Pro Thr His Lys Gly Leu Asn Cys Asn
183      180      185      190
184 Leu Ser Arg Thr Arg His His Asp Glu Pro Gly Asn Ser Asn Met Ser
185      195      200      205
186 Ile Cys Thr Asn Leu Ser Asn Arg Trp Glu Val Phe Gln Ser Ser Ile
187      210      215      220
188 Phe Gly Ala Phe Ala Val Tyr Leu Val Val Leu Ala Ser Val Ala Phe
189 225      230      235      240
190 Met Cys Trp Asn Met Met Lys Val Leu Met Lys Ser Lys Gln Gly Thr
191      245      250      255
192 Leu Ala Gly Thr Gly Pro Gln Leu Gln Leu Arg Lys Ser Glu Ser Glu
193      260      265      270
194 Glu Ser Arg Thr Ala Arg Arg Gln Thr Ile Ile Phe Leu Arg Leu Ile
195      275      280      285
196 Val Val Thr Leu Ala Val Cys Trp Met Pro Asn Gln Ile Arg Arg Ile
197      290      295      300
198 Met Ala Ala Ala Lys Pro Lys His Asp Trp Thr Arg Thr Tyr Phe Arg
199 305      310      315      320
200 Ala Tyr Met Ile Leu Leu Pro Phe Ser Asp Thr Phe Phe Tyr Leu Ser
201      325      330      335
202 Ser Val Val Asn Pro Leu Leu Tyr Asn Val Ser Ser Gln Gln Phe Arg
203      340      345      350
204 Lys Val Phe Trp Gln Val Leu Cys Cys Arg Leu Thr Leu Gln His Ala
205      355      360      365
206 Asn Gln Glu Lys Arg Gln Arg Ala Arg Phe Ile Ser Thr Lys Asp Ser
207      370      375      380
208 Thr Ser Ser Ala Arg Ser Pro Leu Ile Phe Leu Ala Ser Arg Arg Ser
209 385      390      395      400
210 Asn Ser Ser Ser Arg Arg Thr Asn Lys Val Phe Leu Ser Thr Phe Gln
211      405      410      415
212 Thr Glu Ala Lys Pro Gly Glu Ala Lys Pro Gln Pro Leu Ser Pro Glu
213      420      425      430
214 Ser Pro Gln Thr Gly Ser Glu Thr Lys Pro Ala Gly Ser Thr Pro Glu

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215          435          440          445
216 Asn Ser Leu Gln Glu Gln Glu Val
217          450          455
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221 <211> LENGTH: 1368
222 <212> TYPE: DNA
223 <213> ORGANISM: Mouse
225 <400> SEQUENCE: 7
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227 cctgaatttg aggtggccac ttggatcaaa atcaccctca tcttgggtgta cctgatcatt 120
228 tttgtggtag gcatcttggg caacagcgctc accatcaggg ttacgcaggt attgcagaag 180
229 aagggctatt tgcagaagga ggtgacagat cacatgggtca gtttggcttg ttcagatata 240
230 ttgggtctttt tgattggcat gcccatggag ttctacagca tcatttggaa cccctgacc 300
231 acaccagct atgctctgtc ctgtaagctc cacacgttcc tctttgagac gtgcagctac 360
232 gccacactgc tgcacgtgct gaccctcagc tttgagcgct acattgccat ttgtcatccc 420
233 ttcaagtata aagcagtgtc tggacctcgc caggtgaaac tgctgattgg ctttgtatgg 480
234 gtcacctccg ccctgggtggc actgcctttg ctctttgcca tgggtatcga gtacctctg 540
235 gtaaacgtac ccactcaciaa gggactcaac tgcaacctct ctcgcacccg ccaccacgat 600
236 gaacctggaa actccaatat gtccatctgc acgaacctct ccaaccggtg ggaggtcttc 660
237 cagtccagca tctttggggc ctttgtctgt tacctgggtg tcttggcgctc tgtggttttc 720
238 atgtgttggg atatgatgaa agtgctaata aagagcaagc agggcactct tgcagggacc 780
239 gggccacagc tccagctgag gaagtacagag agtgaggaga gccggacagc aagaagacag 840
240 accatcatat tccctgagact gattgtggtg acgttggccg tgtgttggat gcccaatcag 900
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244 tgccgcctga ctctgcagca tgccaaccaa gagaaacgcc agcgtgcccg cttcatctcc 1140
245 accaaggaca gcaccagctc agcccgagc cccctcatct tcctagcctc ccggcgagct 1200
246 aactcttcct ccaggagaac taacaagggt ttcttaagca cttttcagac tgaggccaag 1260
247 cctggagagg ctaagcccca gcccttgagt cctgagtcac cacagactgg ctcagagacc 1320
248 aaaccagctg ggtccacccc agaaaatagt ttacaggagc aggaagta 1368
250 <210> SEQ ID NO: 8
252 <211> LENGTH: 456
253 <212> TYPE: PRT
254 <213> ORGANISM: Rat
256 <400> SEQUENCE: 8
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259 His Ser His Val Pro Glu Phe Glu Val Ala Thr Trp Ile Lys Ile Thr
260          20          25          30
261 Leu Thr Leu Val Tyr Leu Ile Val Phe Val Val Gly Ile Leu Gly Asn
262          35          40          45
263 Ser Val Thr Ile Arg Val Thr Gln Val Leu Gln Lys Lys Gly Tyr Leu
264          50          55          60
265 Gln Lys Glu Val Thr Asp His Met Ile Ser Leu Ala Cys Ser Asp Ile
266          65          70          75          80
267 Leu Val Phe Leu Ile Gly Met Pro Met Glu Phe Tyr Ser Ile Ile Trp
268          85          90          95
269 Asn Pro Leu Thr Thr Pro Ser Tyr Ala Leu Ser Cys Lys Leu His Thr

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VERIFICATION SUMMARY

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